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Escherichia coli 1-176-05_S1_C2, whole genome shotgun sequencing project

NCBI Reference Sequence: [NZ_JJMA00000000.1](#)

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 This entry is the master record for a whole genome shotgun sequencing project and contains no sequence data.

Go to: 

LOCUS NZ_JJMA01000000 5150322 bp DNA linear BCT 22-FEB-2020
DEFINITION Escherichia coli 1-176-05_S1_C2, whole genome shotgun sequencing project.
ACCESSION NZ_JJMA00000000
VERSION NZ_JJMA00000000.1
DBLINK BioProject: [PRJNA224116](#)
BioSample: [SAMN02680133](#)
Assembly: [GCF_000627905.1](#)
KEYWORDS WGS; RefSeq.
SOURCE Escherichia coli 1-176-05_S1_C2
ORGANISM [Escherichia coli 1-176-05_S1_C2](#)
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia.
REFERENCE 1 (bases 1 to 5150322)
AUTHORS Silbergeld,E., Coles,C., Seidman,J.C., You,Y., George,J., Nadendla,S., Huot,H., Daugherty,S.C., Nagaraj,S., Ott,S., Klega,K. and Rasko,D.
TITLE Genetic Variability of E. coli after antibiotic treatment
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 5150322)
AUTHORS Silbergeld,E., Coles,C., Seidman,J.C., You,Y., George,J., Nadendla,S., Huot,H., Daugherty,S.C., Nagaraj,S., Ott,S., Klega,K. and Rasko,D.
TITLE Direct Submission
JOURNAL Submitted (26-MAR-2014) Institute for Genome Sciences, University of Maryland School of Medicine, BioPark II, 801 W. Baltimore St., Suite 619, Baltimore, MD 21201, USA
COMMENT [REFSEQ INFORMATION](#): The reference sequence was derived from [JJMA00000000](#).
The Escherichia coli 1-176-05_S1_C2 whole genome shotgun (WGS) project has the project accession NZ_JJMA00000000. This version of the project (01) has the accession number NZ_JJMA01000000, and consists of sequences JJMA01000001-JJMA01000171.
Bacteria and source DNA available from BEI.

##Genome-Assembly-Data-START##
Assembly Method :: MaSuRCA v. 2.0.3.1
Genome Coverage :: 154.14x
Sequencing Technology :: Illumina
##Genome-Assembly-Data-END##

##Genome-Annotation-Data-START##
Annotation Provider :: NCBI RefSeq
Annotation Date :: 02/22/2020 10:17:07
Annotation Pipeline :: NCBI Prokaryotic Genome Annotation Pipeline (PGAP)
Annotation Method :: Best-placed reference protein set; GeneMarkS-2+
Annotation Software revision :: 4.11
Features Annotated :: Gene; CDS; rRNA; tRNA; ncRNA; repeat_region
Genes (total) :: 5,089
CDSs (total) :: 4,892
Genes (coding) :: 4,641
CDSs (with protein) :: 4,641
Genes (RNA) :: 197
rRNAs :: 10, 6, 7 (5S, 16S, 23S)
complete rRNAs :: 9, 1 (5S, 16S)
partial rRNAs :: 1, 5, 7 (5S, 16S, 23S)
tRNAs :: 154
ncRNAs :: 20
Pseudo Genes (total) :: 251
CDSs (without protein) :: 251
Pseudo Genes (ambiguous residues) :: 0 of 251
Pseudo Genes (frameshifted) :: 99 of 251
Pseudo Genes (incomplete) :: 142 of 251
Pseudo Genes (internal stop) :: 38 of 251
Pseudo Genes (multiple problems) :: 24 of 251
CRISPR Arrays :: 2
##Genome-Annotation-Data-END##

FEATURES
source Location/Qualifiers
1..5150322
/organism="Escherichia coli 1-176-05_S1_C2"
/mol_type="genomic DNA"
/strain="1-176-05_S1_C2"
/isolation_source="stool"
/host="Homo sapiens"
/db_xref="taxon:[1444078](#)"
/country="Tanzania"
/collection_date="13-Jan-2009"
WGS [JJMA01000001-JJMA01000171](#)
WGS_SCAFLD [NZ_JJMA01000001-NZ_JJMA01000171](#)
//

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